tion with one of the Ebola virus strains. It first appeared in 1976 and since then, there is no licensed treatment proven to counteract the virus but various immunological and drug therapies are under development. However, currently two potential candidates are undergoing evaluation. In view of the fact that virtual screening (VS) is an increasingly used method to guide the identification of novel hits from large chemical libraries.

Methods & Materials: Selection of Series with activity range span above 3.0 orders Hypothesis generation Using Hypogen module of Discovery Studio Followed by Model Validation and Virtual Screening Molecular docking studies to understand the type of molecular interactions within the active site of target using LibDocker/CDocker modules of Discovery Studio Biological Studies (In-Vitro/In-Vivo) to test the activity of the retrieved lead compounds

Results: We have tried to propose a research work which is structure and ligand based pharmacophore generation and chemical compound database mining (*In-silico* high throughput screening) followed by molecular docking to retrieve potent structurally diverse anti-Ebola drugs. The identified compounds will be further subjected to *in- vivo*/*in-vitro* studies. The identified compounds will be further subjected to *in- vivo*/*in-vitro* studies.

Conclusion: Reducing the research timeline in the drug discovery stage is a main concern worldwide. Various *In silico* techniques offering economical methods are now being used for the drug development. Molecular modelling is emerging as a popular methodology for drug design which aims at computer-aided techniques for the efficient identification and optimization of novel compounds with a required biological activity. Moreover, virtual screening is also a reliable and economical method as it helps in identification of new molecules which share its features and can thus exhibit a desired biological response. In view of the role of In-silico drug designing, the aim of the proposed research entitled "***Pharmacophore Modeling, Database Mining and Biological Evaluation to Identify Novel Structurally Diverse compounds as Potential anti- Ebola drugs"*** is to elucidate the structural features responsible for anti-Ebola activity and to identify novel potential leads as anti-Ebola drugs.

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West Nile Virus circulation and incrimination of mosquito vectors in Northeast India

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Background: West Nile virus (WNV) is a flavivirus transmitted by mosquitoes. The prevalence of WNV antibodies in Indian population has been known since 1952. Following phylogenetic analysis, Indian isolates were classified into Lineage 1 and 5. Since 2006, with the identification of WNV as an aetiology causing acute encephalitis syndrome (AES) in Northeast India, scattered cases have been recorded in Assam every year during the months of June to October. However, the mosquito species involved in transmission of WNV in this region requires detailed study.

Methods & Materials: We analysed human sera from hospitalised AES cases and mosquitoes sampled in four West Nile reporting areas during June 2014 - June 2015. Mosquitoes were caught using suction tube and flash light. A total of 970 pools from 37246 mosquitoes were based on uniformity of species, collection site and date. Clinical samples were tested for presence of WNV-specific IgM antibodies and confirmed by neutralizing antibody test for the acute and convalescent phase serum specimen. Both clinical samples and mosquito pools were also tested for the presence of WNV RNA using NS1 gene specific primers.

Results: Of the 222 AES acute case serum samples tested for the presence of WNV specific IgM antibodies, 48 were found positive. Six IgM positive samples demonstrated a fourfold rise in neutralizing antibody titre against WNV in convalescent sera. WNV RNA was detected in the cerebrospinal fluid of one human sample. Vector incrimination showed 14 pools (4- *Culex vishnui*, 1- *Culex pseudovishnui*, 2- *Culex tritaeniorhynchus*, 2- *Culex quinquefasciatus*, 1- *Culex whitmorei* and 4 -*Mansonia uniformis)* to be positive for WNV RNA. Interestingly, 13 of the positive pools were collected during November- December 2014. Mosquito and human derived WNV sequence were similar to Indian Lineage 5 WNV isolates.

Conclusion: Our results provide molecular evidence for the persistence and maintenance of Lineage 5 WNV in Northeast India. This study confirms the role of *Culex and Mansonia* mosquito species in the transmission of WNV in Assam. Further studies are required to address WNV transmission and maintenance during winters for implementation of vector intervention strategies.

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Molecular phylogenetics of Orientia tsutsugamushi strains circulating in Assam based on 56-kilodalton type-specific antigen gene

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Background: In India, scrub typhus (ST) is considered to be a re-emerging infectious disease. From northeast India, ST cases have recently been reported (2012) in Assam after a gap of 68 years. The causative organism, Orientia tsutsugamushi is known to be genetically and antigenically highly variable. Sequence analysis of 56-kilodalton (kda) type-specific antigen (TSA) gene has become an important tool for genetic characterization of Orientia. This variable gene sequence is useful for analysis of genetic diversity of Orientia isolates. Although re-emergence of ST has been reported, circulating strains and their origin have yet to be identified. In the present

study, we determined the prevalent strains of O. tsutsugamushi circulating in Assam and their origin with respect to 56 kDa TSA gene.

Methods & Materials: 370 clinical serum samples from suspected scrub typhus and other unidentified fever cases were received from tertiary hospitals in Assam. Serological screening was done using Scrub Typhus Detect IgM ELISA (InBios International, Inc., USA). Positive and equivocal samples were subjected to PCR. Nested PCR was performed using primers specific for O. tsutsugamushi 56 kDa gene. Phylogenetic analysis was performed using MEGA 6 software.

Results: 19.4% sera (72/370) were found to be IgM positive and 6.4% (24/370) were equivocal. 13 of these samples were PCR positive for 56 kDa gene. Phylogenetic analysis of study strains showed variations in sequence homologies that formed 3 distinct clades that clustered with reference strains from: 1) India 2) Taiwan and 3) Thailand.

Conclusion: In summary, we have identified strains of O. tsutsugamushi circulating in Assam and established their evolutionary relationship with reference strains by analyzing a variable portion of 56 kDa gene. Understanding the evolution of the prevalent strains is important to understand the genetic differences which may help in planning control strategies as well as prophylactic measures including development of vaccines.

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Uganda National Acute Febrile Illness Agent Detection Serosurvey 2004-2005

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Background: Due to their non-specific clinical presentation, acute febrile illnesses (AFI) are often diagnosed clinically as diseases known to be endemic to the region in which they are found. Uganda has been the site of multiple emerging-disease outbreaks, and there are several diseases that present with undifferentiated AFI, requiring further laboratory confirmation; however, limited laboratory capacity can impair timely diagnosis and public health interventions. This results in misdiagnosis and underreporting of emerging diseases of public health importance. The 2004-2005 Uganda National AFI Agent Detection Serosurvey (AFI serosurvey)–a retrospective investigation of seroprevalence of exposure to selected infectious agents–involved testing a subset of banked sera from the 2004-2005 Uganda HIV/AIDS Serobehavioural Survey (UHSBS). The AFI serosurvey is part of a multi-phase collaboration between Uganda Ministry of Health, Uganda Virus Research Institute (UVRI) and CDC-Atlanta/CDC-Uganda to investigate AFI in Uganda.

Methods & Materials: We selected a random 3097-sample subset from 19,656 UHSBS banked sera for inclusion in the AFI serosurvey; 2705 were ultimately analyzed after applying exclusion criteria. Data from laboratory testing were analyzed and mapped using SAS v9.3 and ArcGIS 10, respectively.

Results: Laboratory diagnostic testing results demonstrated: leptospirosis ELISA and microagglutination test (MAT) (10.4% weighted proportion, SE = 1.2%), brucellosis MAT (0.3% weighted proportion, SE = 0.1%), spotted fever group rickettsiae ELISA (56.7% weighted proportion, SE = 1.4%) and typhus group rickettsiae ELISA (41.6% weighted proportion, SE = 1.4%), malaria MSP119 ELISA (88.4% weighted proportion, SE = 0.7%), orthopoxvirus IgG ELISA (13.5% weighted proportion, SE = 0.8%), chikungunya IgM ELISA (31.1% weighted proportion, SE = 1.0%), dengue IgM ELISA (1.0% weighted proportion, SE = 0.2%) and IgG ELISA (0.7% weighted proportion, SE = 0.2%). A specimen subset (n = 198) was tested for melioidosis using indirect hemagglutination (IHA); 4.6% were seropositive.

Conclusion: Pre-existing national serosurveys can be a source of information on prevalence of AFI etiologic agents. This AFI serosurvey describes the distribution, regional risk, and interregional variability for selected diseases contributing to AFI across Uganda; it will inform prioritization of infectious disease surveillance and laboratory capacity-building activities. Results from this study combined with similarly obtained results from the ongoing testing from the 2011 Uganda AIDS Indicator Survey-based serosurvey will demonstrate changing seroprevalence patterns, allowing for evaluation of potential ecologic drivers for disease distribution variances.

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Spotted fever group and typhus fever group rickettsiosis in South Western India

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Background: Rickettsial diseases are a group of zoonotic acute febrile illness transmitted to humans by vectors. They are classified into spotted fever group (SFG), typhus fever group (TG) and scrub typhus group (STG). STG remains the major cause of acute febrile illness requiring hospitalization in the tsutsugamushi triangle, however, the true picture of the SFG and TG rickettsiosis is not clear in India. Immunofluorescence assay (IFA) is the serological gold standard test for the diagnosis of rickettsial disease and